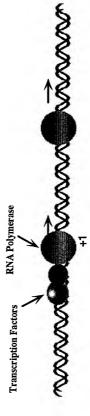


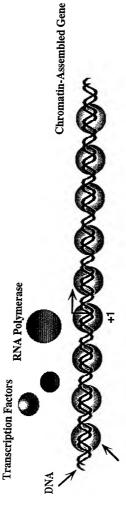
Figure 2 ACTIVE GENE



 Transcription Factors and RNA Polymerase interact with promoter region

2. RNA Polymerase moves down the gene to read or "transcribe" the DNA coding sequence and produce mRNA

Figure 3 INACTIVE GENE (in Chromatin)



Nucleosome (basic unit of chromatin) (composed of DNA + histone proteins)

INACTIVE GENE

Nucleosomes block accessibility of Transcription Factors and RNA Polymerase to DNA; Proteins cannot interact with promoter region to activate gene

Figure 4 ACTIVE GENE (in Chromatin)

Chromatin-Assembled Gene Remodeling Complex +ATP

Transcription Factors, RNA Polymerase

ACTIVE GENE

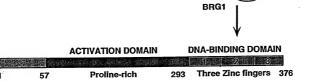
Remodeling Complex (SWL/SNF, etc.) is targeted by Transcription Factor and "loosens" nucleosomal structure to facilitate interaction of Transcription Factor and RNA Polymerase with promoter DNA which activates the gene.

SWI/SNF Chromatin Remodeling Complex

	ACTIVATION DO	MAIN DNA-BINDING DOMAIN
	Maria Maria	20 4822 1932
1 57	Proline-rich	293 Three Zinc fingers 376

Figure 5

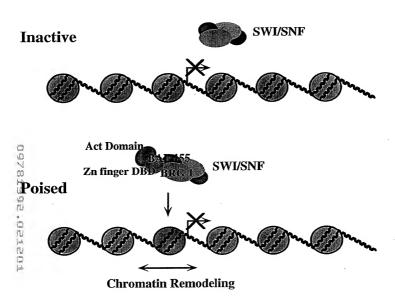
Chromatin Remodeling Complex

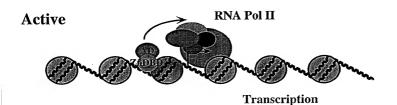


SWI/SNF minimal complex

Figure 6

POSSIBLE MECHANISM OF SWI/SNF-DEPENDENT CHROMATIN REMODELING BY IN ERACTION WITH ZINC-FINGER DNA BINDING PROTEINS





β-globin ഺ	GATA-1	GATA-1	EKLF	CATA	->	Fig8
	-200	-120	-90	-30	+1	

19 293 376
EKLF DBD
(Zn++ Finger)